

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 22:15:02 ; Search time 5994 Seconds
(without alignments)
4808.662 Million cell updates/sec

Title: US-10-029-345A-109

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Searched: 3470272 seqs, 21671516995 residues

Word size: 473

Total number of hits satisfying chosen parameters: 2

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Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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DEFINITION Sequence 108 from Patent WO02057460.
ACCESSION AX482439
VERSION AX482439.1 GI:22316984
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Todderud C.G., Bol D., Pinger J., Lee L., Nelson T., Schieven G., Suchard S., Banas D., Basolino D., Feder J., Krytek S., Wcatree P., Mintier G., Siemers N., Jackson D.G. and Ramachan C.
TITLE Polynucleotides encoding human phosphatases
JOURNAL Patent: WO 02057460-A 108 25-JUL-2002;
SQUIBB BRISTOL MYERS CO (US)
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DEFINITION Sequence 147 from Patent WO2057460.
ACCESSION AX482478
VERSION AX482478.1 GI:22316999
KEYWORDS
SOURCE
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REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Suchard,S., Banae,D., Bassolino,D., Feder,J., Krysek,S.,
Mcatee,P., Minter,G., Siemers,N., Jackson,D.G. and Kamanathan,C.
JOURNAL Polynucleotides encoding human phosphataases
Patent: WO 02057460-A 147 25-JUL-2002;
SQUIBB BRISTOL MYERS CO (US)
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LOCUS AX482478 5450 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 147 from Patent WO2057460.
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VERSION AX482478.1 GI:22316999
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
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TITLE Todderd,C.G., Bol,D., Finger,J., Lee,L., Nelson,T., Schieven,G.,
Suchard,S., Banae,D., Bassolino,D., Feder,J., Krysek,S.,
Mcatee,P., Minter,G., Siemers,N., Jackson,D.G. and Kamanathan,C.
JOURNAL Polynucleotides encoding human phosphataases
Patent: WO 02057460-A 147 25-JUL-2002;
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Search completed: June 24, 2004, 01:46:29
Job time : 6003 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 19:31:01 ; Search time 615 Seconds
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Title: US-10-029-345A-109

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Scoring table:
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Ygapop 60.0 , Ygapext 60.0
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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N Geneseq.29Jan04:*
1: geneseqn19806:*
2: geneseqn19906:*
3: geneseqn20006:*
4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2003a:*
8: geneseqn2003b:*
9: geneseqn2003c:*
10: geneseqn2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	665	100.0	5450	6	ACCG0559 Polynucle
2	665	100.0	5450	6	ACCG0572 Polynucle

ALIGNMENTS

RESULT 1
ACCG0559

ID ACCG0559 strand; cDNA; 5450 BP.
ACCG0559;
19-JUN-2003 (first entry)
DE Polynucleotide relating to the invention SEQ ID NO: 108.
XX Gene; ss; antiproliferative; hepatotropic; nephrotropic; antiarthritic;
XX antipsoriatic; cardiant; cyostatic; gene therapy; liver disease;
XX proliferative disorder; renal failure; cardiovascular disorder;
XX immunological disorder; arthritis; psoriasis; congenital heart defect;
XX congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.
XX Homo sapiens.
OS
PN WO200257460-A2.
XX
PD 25-UTL-2002.
XX
PF 20-DEC-2001; 2001WO-US050459.
XX
PR 20-DEC-2000; 2000US-0256868P.
XX
PR 30-MAR-2001; 2001US-0280186P.
XX
PR 01-MAY-2001; 2001US-0287735P.
XX
PR 05-JUN-2001; 2001US-0295848P.
XX
PR 25-JUN-2001; 2001US-0300465P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L;
PI Stiemers N, Boi D, Schieven G, Finger J, Todderud CG, Bassolino D;
PI Krystek S, Mcatee P, Suchard S, Banas D;
XX
DR WPI; 2002-599721/64.
XX
DR P-PDSB; ABR52381.
XX
PT Novel polynucleotides encoding human phosphatase polypeptides useful in
XX the prevention or treatment of e.g. proliferative and cardiovascular
XX disorders.
XX
PS Claim 1; Fig 13; 801pp; English.
XX
XX The invention relates to a novel isolated nucleic acid comprising a
XX polynucleotide having a nucleotide sequence selected from 40
XX polynucleotides fully defined in the specification. The polynucleotide of
XX the invention has antiproliferative, hepatotropic, nephrotropic,
XX antiarthritic, antipsoriatic, cardiant, and cyostatic activity. The
XX polynucleotide may have a use in gene therapy. A polynucleotide or
XX polypeptide of the invention is useful for preventing, treating or
XX ameliorating a medical condition, e.g. a proliferative disorder. They are
XX also useful for treating e.g. liver disease, renal failure, immunological
XX disorders including arthritis and psoriasis, cardiovascular disorders
XX such as congenital heart defects and congestive heart failure, and
XX cancer. A method of the invention is useful for diagnosing a pathological
XX condition or susceptibility to a condition in a subject. The present
XX sequence is used in the exemplification of the invention
XX
SQ Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0 Length: 5450
Score: 665.00 Matches: 665
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-345A-109 (1-665) x ACCG0559 (1-5450)
Qy 1 MetaLahieGJumetIlegIyThrgInIeva1ThrgIuArgIeuValAlaleuLeugIu 20
Db 538 ATGGCCCATGACATGATTGGAACTCAATTGTTACTGAGAGAGTGGCTGCTGCGAA 597

QY 21 SerGIYThrGIuLysValLeuLeuIleAspSerArgProPheValGIuTYrAsnThrSer 40
 Db 598 AGTGAAGCGAAGAAAGTCTGTATATGATAGCCGGCATTTGGAAATACAAATACATCC 657
 QY 41 HisIleLeuGIuAlaIleAsnIleAspCysSerIleuMetLysArgArgLeuGIuGln 60
 Db 658 CACATTTTGAAGACCATTAATATCACTGCTCCAGCTTATGAAAGCGAAGGTGCACACG 717
 QY 61 AspLysValLeuIleThrGIuLeuIleGlnHisSerAlaLysSHisLysValAspIleAsp 80
 Db 718 GACAAAGGTAAATTAACAGACTCATCCAGCATTCAGGAAACATTAAGTTGACATTGAT 777
 QY 81 CysSerGIuLysValValValTYrAspGlnSerSerGIuAspValAlaSerLeuSerSer 100
 Db 778 TGCAGTCGAAGAGTTGATGTTACGATCAAGCTCCCAAGATGTGCTCTCTCTTCA 837
 QY 101 AspCysPheLeuThrValLeuLeuGIuLysLeuGIuLysSerPheAsnSerValHisLeu 120
 Db 838 GACTGTTTCTCACGTACTTCTGGGTAACTGGAGAAGACTTCACACTCTGTTCACTG 897
 QY 121 LeuAlaGIuGIuPheAlaGIuPheSerArgCysPheProGIuLeuCysGIuGIuLysSer 140
 Db 898 CTTCCAGGTGGTTGCTGAGTCTCTGTTGTTCCCTGGCTCTGTGAAGAAATCC 957
 QY 141 ThrLeuValProThrCysIleSerGIuProCysLeuProValAlaAsnIleGIuProThr 160
 Db 958 ACTTTAGTCTTACCTGATTTCTCAGCTTCTGCTTACCTGTGGCAATTGGGGCAACC 1017
 QY 161 ArgIleLeuProAsnLeuTYrLeuGIuLysGlnArgAspValLeuAsnLysGIuLeuIle 180
 Db 1018 CGAATCTTCCCATCTTATCTTGGCTGCAGAGATGCTCCCAAGAGACTATA 1077
 QY 181 GlnGlnAsnGIuIleGIuTYrValLeuAsnAlaSerTYrThrCysProLysProAspPhe 200
 Db 1078 CAGAGAGATGGATGTGTATGTGTTAAATGCCAGCTATACCTGTCCAAAGCCGACTTT 1137
 QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGIuLysIleLeu 220
 Db 1138 ATCCCGAGCTCACTTCTCGCGCTGCTGTGAATACAGCTTTGTGGAATAATTTTG 1197
 QY 221 ProTYrLeuAspLysSerValAspPheIleGIuLysAlaLysAlaSerAsnGIuCysVal 240
 Db 1198 CCGGTGTGGACAATCAGTAGATTTCTATGAGAAACAAAGCCTCATGATGTTG 1257
 QY 241 LeuValHisCysLeuAlaGIuIleSerArgSerAlaThrIleAlaIleAlaTYrIleMet 260
 Db 1258 CTAGTGCACTGTTAGCTGGGATCTCCGCTCGCCACCAATCGCTATCGCTCATCATC 1317
 QY 261 LysArgMetAspMetSerLeuAspGIuAlaTYrArgPheValLysGIuLysArgProThr 280
 Db 1318 AAGGAGATGACATGCTTTAGATGAAGCTTACAGATTGTGAAAGAAAACCTACT 1377
 QY 281 IleSerProAsnPheAsnPheLeuGIuLysLeuAspTYrGIuLysIleLysAsn 300
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 QY 301 GlnThrGIuAlaSerGIuProLysSerLysLeuLysLeuMetHisLeuGIuLysProAsn 320
 Db 1438 CAGACTGAGCATCAGGGCCAAAGAGCAATCAAGCTGCTGCACTGGAGAAAGCCAAAT 1497
 QY 321 GluProValProAlaValSerGIuGIuLysSerGIuLysProLeuSerProPro 340
 Db 1498 GAACCTGTCTCTGCTCAGAGGGGTGACAGAAAGAGAGAGCCCTCAGTCAACC 1557
 QY 341 CysAlaAspSerAlaThrSerGIuAlaAlaGIuLysArgProValHisProAlaSerVal 360
 Db 1558 TGTGCCGACTCTCTACCTCAGAGCAGCAGCAAAAGGCCCTGTGATCCCGCAGCGTG 1617
 QY 361 ProSerValProSerValGlnProSerLeuLeuGIuAspSerProLeuValGlnAlaLeu 380
 Db 1618 CCAAGCTGCCAGCTGACGCTGCTGTGTTAGAGACACGCCGCTGTACAGGCGCTC 1677

QY 381 SerGIuLysIleuSerAlaAspArgLeuGIuAspSerAsnLysLeuLysArgSerPhe 400
 Db 1678 AGTGGCTGCACCTGTCCGACAGAGCTGGAGAGACGAATAGCTCAAGCGTCTTC 1737
 QY 401 SerLeuAspIleLysSerValSerTYrSerAlaSerMetAlaAspLeuHisGIuPhe 420
 Db 1738 TCTTGATATCAAAATCAATGTTATATATCAAGCAGATGGACATCTTACATGGCTTC 1797
 QY 421 SerSerGIuAspAlaLeuGIuTYrTYrLysProSerThrThrLeuAspGIuThrAsn 440
 Db 1798 TCTTCATCAGAAATGCTTTGGAATACTCAAACTTCCACTTCTGTGATGGAGCAAC 1857
 QY 441 LysLeuCysGlnPheSerProValGlnGlnLeuSerGIuGlnThrProGIuThrSerPro 460
 Db 1858 AAGCTATGCCAGTTCTCCCTGTTCAGGAATATCGAGACAGCTCCCAAAACCACTCCT 1917
 QY 461 AspLysGIuGIuAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
 Db 1918 GATTAAGAGAGAACCCAGCATCCCAAGAAAGCTGCAGACCGCCAGGCTTCAGACACCA 1977
 QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGIuTYrAlaGlnArgSerLeuLeu 500
 Db 1978 AGCAAGCATTTGCATTCTGGTCAGAACCAAGCAGAGTGCGACCGCCAGAGGTCCCTTTA 2037
 QY 501 SerProLeuHisArgSerGIuSerValGIuAspAsnTYrHisThrSerPheLeuPheGIu 520
 Db 2038 TCTTCACCTCATCGAAGTGGAGCGGTGAGACAAATTAACACAGACTTCTTTTCGGC 2097
 QY 521 LeuSerThrSerGIuGlnHisLeuTYrLysSerAlaGIuLysGIuLysArgTYrPheHis 540
 Db 2098 CTTTCCACAGCAGCAGAGCACTCAAGATCTGTGCTGGCTTGAAGGCTGGCAC 2157
 QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTYrPheAla 560
 Db 2158 TCGAATATCTTGGCCCCCAGACCTTCACTTCCTGAGCAGAGCTGATATTTGGC 2217
 QY 561 ThrGlnSerSerHisPheTYrSerAlaSerAlaIleTYrGIuLysSerAlaSerTYrSer 580
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 QY 581 AlaTYrSerCysSerGIuLeuProThrCysGIuAspGlnValTYrSerValArgArg 600
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 QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTPheGIuGlnSerProPheGln 620
 Db 2338 CAGAAAGCCAAAGACAGAGCTGACCTGGCGGAGCTGGCAGAAAGAGCCCTTTGAA 2397
 QY 621 LysGlnPheLysArgArgSerCysGlnMetGlnPheGIuLysSerIleMetSerGlnAsn 640
 Db 2398 AAGCAGTTTAAACGAGAAAGCTGCCAAATGGAATTTGAGAGAGCATCATGTCAAGAAC 2457
 QY 641 ArgSerArgGIuGlnLeuGIuLysValGIuLysSerGlnSerSerPheSerGIuMetGln 660
 Db 2458 AGGTACCGGAAGACCTGGGGAAGTGGGAGTCAAGTCACTTTTCCGCGAGCATGAA 2517
 QY 661 IleIleGIuValSer 665
 Db 2518 ATCATTAAGTCTCC 2532

RESULT 2
 ACC60572
 ID ACC60572 standard; cDNA, 5450 BP.
 XX
 AC ACC60572;
 XX
 XX 19-JUN-2003 (first entry)
 DT
 XX
 DE Polynucleotide relating to the invention SEQ ID NO: 147.
 XX
 KW Gene; ss; antiproliferative; hepatotropic; nephrotropic; antiarthritic;
 KW antiproliferative; cardiant; cytostatic; gene therapy; liver disease;
 KW proliferative disorder; renal failure; cardiovascular disorder;

KM immunological disorder; arthritis; psoriasis; congenital heart defect;
KW congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.
XX Homo sapiens.
XX MO200257460-A2.
XX
XX 25-JUL-2002.
XX
XX 20-DEC-2001; 2001MO-US050459.
XX
XX 20-DEC-2000; 2000US-0256868P.
XX 30-MAR-2001; 2001US-0280186P.
XX 01-MAY-2001; 2001US-0287735P.
XX 05-JUN-2001; 2001US-0295848P.
XX 25-JUN-2001; 2001US-0300465P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Jackson DG, Feder J, Nelson T, Mintler G, Ramanathan C, Lee L,
XX Stewers N, Bol D, Schieven G, Finger J, Todderud CG, Basolino D,
XX Krysatek S, Mcatee P, Suchard S, Banas D;
XX MPI; 2002-599721/64.
XX P-PSDB; ABR52407.
XX
XX Novel polynucleotides encoding human phosphatase polypeptides useful in
XX the prevention or treatment of e.g. proliferative and cardiovascular
XX disorders.
XX
XX Example 7; Fig 19; 801pp; English.
XX
XX The invention relates to a novel isolated nucleic acid comprising a
XX polynucleotide having a nucleotide sequence selected from 40
XX polynucleotides fully defined in the specification. The polynucleotide of
XX the invention has antiproliferative, hepatotropic, nephrotropic, CC
XX antidiabetic, antipsoriatic, cardiant, and cytostatic activity. The
XX polynucleotide may have a use in gene therapy. A polynucleotide or
XX polypeptide of the invention is useful for preventing, treating or
XX ameliorating a medical condition, e.g. a proliferative disorder. They are
XX also useful for treating e.g. liver disease, renal failure, immunological
XX disorders including arthritis and psoriasis, cardiovascular disorders
XX such as congenital heart defects and congestive heart failure, and
XX cancer. A method of the invention is useful for diagnosing a pathological
XX condition or susceptibility to a condition in a subject. The present
XX sequence is used in the exemplification of the invention
XX
XX Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0 Length: 5450
XX Score: 665.00 Matches: 665
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: Gaps: 0
XX
XX US-10-029-345A-109 (1-665) x ACC60572 (1-5450) .
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XX DB 538 ATGGCCCATGAGATGATGGAACTCAATGTTAATGAGAGTGGGCTGCTGGGAA 597
XX QY 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
XX DB 598 AGTGGAAAGGAAAGAGTCTGCTAATGATGACCGGCAATTTGTGAAATCAATACATCC 657
XX QY 41 HisIleLeuGluValIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
XX DB 658 CACATTTGGAAAGCACTTAATATCACTGCCAAGCTTATGAAGCAAGGTTGCAACAG 717
XX QY 61 AspLysValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80

DB 718 GACAAAGTGTAAATTAACAGCTCAATCCAGCATTCAGCAAAACATAGGTTGACATTGAT 777
QY 81 CysSerGlnLysValValValIleArgGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB 778 TGCAGTCAGAAAGTGTAGTTAATGATCAAGATCCCAAGATGTTCCCTCTCTCTTCA 837
QY 101 AspCysPheLeuThrValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
DB 838 GACTGTTTCTCAGTACTTCTGGGTAAACTGGAGAAAGCTTCAACTGTTCACCTG 897
QY 121 LeuAlaGlyIlePheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140
DB 898 CTTGCAGTGGGTGCTTCTAGTTCCTCTGTTTCCCTGCTGTGAAAGAAATCC 957
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 958 ACTGATCCCTCACTGCAATTCCTCAGCTTCTCAGCTTCTCAGTCCCAACTGGGCAACC 1017
QY 161 ArgIleLeuProAsnLeuThrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuIle 180
DB 1018 CGAATTCCTCCCAATCTTATCTTGGCTGCCAGCGAATGCTCTCAACAAAGAGCTGATA 1077
QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
DB 1078 CAGCAGAAATGGATTTGTTATGTTAAATGCCAGCTAATCCTGTCCAAAGCTGACTTT 1137
QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLeu 220
DB 1138 ATCCCGAGTCTCATTTCTGCGGTGCTGCGTGAATGACAGCTTTGTGAGAAATTTTG 1197
QY 221 ProThrLeuAspLysSerValAspPheIleGluValAlaLysArgGlyCysVal 240
DB 1198 CCGTGTGTGACAAACATTAATGATTCATTGAGAAAGCAAGCTCCCAATGATGTGT 1257
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
DB 1258 CTAATGCTGTTTAACTGGATCTCCCTCCGCCACCATCCGTATCCCTACATCATG 1317
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGluLysArgProThr 280
DB 1318 AAGAGATGACATGCTTAAATGATGAAGCTTACAGATTGTGAAAGAAAGAAAGACTACT 1377
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysIleLysAsn 300
DB 1378 AATATCCCAACTCAATTTTCTGGGCCCACTCTGAGATGAGAAAGATTAAGAAC 1437
QY 301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGluLysProAsn 320
DB 1438 CAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGCTGCACTGAGAAAGCCAAAT 1497
QY 321 GluProValProAlaValSerGluGlyGlnLysSerGluThrProLeuSerProPro 340
DB 1498 GAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1557
QY 341 CysAlaAspSerAlaThrSerGluValAlaGlyGlnArgProValHisProAlaSerVal 360
DB 1558 TGTGCCGACTCTGCTACCTCAGAGGCAAGCAAGGCGCTGATCCCGCACAGGTG 1617
QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
DB 1618 CCCAGGCTGCCAGCTGCGAGCGGCTGCTGTTAGAGACAGCCGCTGTAAGGGGCTC 1677
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluLysSerAsnLysLeuLysArgSerPhe 400
DB 1678 AGTGGCTCACCTGCTGCCAGACAGCTGGAAGACAGCAATAGCTCAAGCTTCTCTTC 1737
QY 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
DB 1738 TCTCTGATATCAAAACATTTTCAATTCAGGCAAGATGGCAAGCATTTACATGGCTTC 1797
QY 421 SerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440
DB 1798 TCTCTCATCAAGAGATGCTTGGAAATCTAAGAACTTCCACTGATGATGGAGCAAC 1857

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QY 441 LysLeuCyGlnPheSerProValGlnLeuSerGlnGlnThrProGlnThrSerPro 460
Db 1858 AAGCTATGCCAGTTCTCCCTGTTCCAGAACTATCGAGACACTCCGAAACCAAGTCTT 1917
QY 461 AspLysGlnGlnAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
Db 1918 GATTAAGAGGAAGCCAGCATCCCAAGAAAGCTGACAGACCGCAGCTTCACAGACCCAG 1977
QY 491 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db 1978 AGCAAGCGATTGCATTCGGTCAGAACCAAGACAGATGGCACCGCCAGAGGCTCCCTTTTA 2037
QY 501 SerProLeuHisArgSerGlySerValGlnLysAsnTyrHisThrSerPheLeuPheGly 520
Db 2038 TCTCCACTGCATCGAAGTGGAGCGGTGGAGACAATTACACACAGCTTCCTTTTCGGC 2097
QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrHis 540
Db 2098 CTTTCCACCAAGCCAGACACACTCAGAAAGTCTGCTGGGCTTGAAGGCTGGCAC 2157
QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
Db 2158 TCGGATATCTTGGGCCCCCAGACCTTACCCCTTCCCTGACACAGACTGGTATTTGCC 2217
QY 561 ThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSer 580
Db 2218 ACAAGATCTCTACACTTCTACTCTGCTCAGCCCATCTTACGAGGAGAGTGCAGTTACTCT 2277
QY 581 AlaTyrSerCySerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
Db 2278 GCTTACAGCTGACCAAGCTGCCCACTTGGCGAGACCAAGTCTATTTCTGTCCGAGGCG 2337
QY 601 GlnLysProSerAspAlaArgAlaAspSerArgArgSerTyrHisGlnGlnSerProPheGln 620
Db 2338 CAGAAAGCCAAGTGCAGAGCTGACTCGCGGCGAGCTGGCATGAAAGAGAGCCCTTTGAA 2397
QY 621 LysGlnPheLysArgSerCySerGlnMetGlnPheGlyGlnSerIleMetSerGlnAsn 640
Db 2398 AAGCAGTTTAAACCCAGAAAGCTGCCAATGGAATTTGAGAGAGCATCATGTCAAGAAC 2457
QY 641 ArgSerArgGlnGlnLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGln 660
Db 2458 AGGTCAAGGGAAGAGCTGGGGAAGAGTGGCAGTCAAGTCTAGCTTTTGGGCAAGATGAA 2517
QY 661 IleIleGlnValSer 665
Db 2518 ATCATTTAGGCTCTCC 2532
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Search completed: June 24, 2004, 00:04:41
Job time : 624 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 23:00:42 ; Search time 3667 Seconds

(without alignments)
5415.421 Million cell updates/sec

Title: US-10-029-345A-109

Perfect score: 665
Sequence: 1 MAHEMGTQIVTERLVALL.....LKVSGSQSFGSGMERIEVS 665

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Rgapop 6.0 , Rgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Word size: 473

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Command line parameters:

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-Q/cqn2.1/USPTO.spool.p/US10029345/Runat 23062004 121752 25604/app query.fasta_1.839
-DB=EST -QFMT=fastap -SUFFIX=ol12.rst -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human4.cdt -LIST=75
-DOCCALIGN=200 -THR_SCORE=quality -THR_MIN=473 -ALIGN=50 -MODE=LOCAL
-OUTFMT=plco -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
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Database :

EST: *
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2: em_esthum: *
3: em_estin: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
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12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estcom: *
17: em_gss_hum: *
18: em_gss_hiv: *
19: em_gss_pln: *
20: em_gss_vrt: *
21: em_gss_fun: *
22: em_gss_man: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rtd: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gss1: *

29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
No matches found					

Search completed: June 24, 2004, 02:47:42
Job time : 3667 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 23:54:21 ; Search time 666 Seconds
(without alignments)
4574.211 Million cell updates/sec

Title: US-10-029-345A-109
Perfect score: 665
Sequence: 1 NAHEMIGTGYTERLVALL.....LAKVGSQSFSGSMETIEVS 665

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2230544650 residues

Word size: 473

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human0.cgi -LIST=75 -DOCCALIGN=200 -THR_SCORE=quality -THR_MIN=473
-ALIGN=50 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10029345 @CGN 1 1 723 @runat 23062004 121753 25636
-NGPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGIOQ -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-Fgapop=6 -Fgapext=7 -Ygapop=60 -Ygapext=60 -DELOP=6 -DELEX=7

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Query Length	DB ID	Description
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No matches found

Search completed: June 24, 2004, 03:01:36
Job time : 666 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 23:25:13 ; Search time 139 Seconds
(without alignments)
2654.981 Million cell updates/sec

Title: US-10-029-345A-109

Perfect score: 665
Sequence: 1 MAHEMIGTQIVTERLVALLIE.....LGRVGSQSSFGSGMEIIEVS 665

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Word size: 473

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q/cgn2_1/uspto.spool.p/us10029345/runat.23062004.121753.25617/app.query.fasta_1.839
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=oli2.rn1 -MINMATCH=0.1 -LOOPCL=0
-LIST=75 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=473 -ALIGN=50 -MODE=LOCAL
-OUTFMT=plc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10029345 @CGN 1 1 105 @runat.23062004.121753.25617 -NCPU=6 -ICPU=3
-NO MAP -LARGEDEV -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description

No matches found				

Search completed: June 24, 2004, 02:50:16
Job time : 139 secs

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